SEQUENCE LISTING

<110> Mark J. Graham
      Andrew T. Watt

<120> ANTISENSE MODULATION OF COMPLEMENT COMPONENT C3 EXPRESSION

<130> RTS-0329

<160> 179

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Met Gly Pro Thr Ser Gly Pro Ser Leu Leu Leu Leu Leu Thr His
1   5   10   15

ctc ccc ctg gct ctg ggg agt ccc atg tac tct atc atc acc ccc aac   156
Leu Pro Leu Ala Leu Gly Ser Pro Met Tyr Ser Ile Ile Thr Pro Asn
                20   25   30

atc ttg cgg ctg gag agc gag gag acc atg gtg ctg gag gcc cac gac   204
Ile Leu Arg Leu Glu Ser Glu Glu Thr Met Val Leu Glu Ala His Asp
            35   40   45

gcg caa ggg gat gtt cca gtc act gtt act gtc cac gac ttc cca ggc   252
Ala Gln Gly Asp Val Pro Val Thr Val Thr Val His Asp Phe Pro Gly
        50   55   60

aaa aaa cta gtg ctg tcc agt gag aag act gtg ctg acc cct gcc acc   300
Lys Lys Leu Val Leu Ser Ser Glu Lys Thr Val Leu Thr Pro Ala Thr
65   70   75   80

aac cac atg ggc aac gtc acc ttc acg atc cca gcc aac agg gag ttc   348
Asn His Met Gly Asn Val Thr Phe Thr Ile Pro Ala Asn Arg Glu Phe
                85   90   95

aag tca gaa aag ggg cgc aac aag ttc gtg acc gtg cag gcc acc ttc   396
Lys Ser Glu Lys Gly Arg Asn Lys Phe Val Thr Val Gln Ala Thr Phe
                100   105   110

ggg acc caa gtg gtg gag aag gtg gtg ctg gtc agc ctg cag agc ggg   444
Gly Thr Gln Val Val Glu Lys Val Val Leu Val Ser Leu Gln Ser Gly
            115   120   125

tac ctc ttc atc cag aca gac aag acc atc tac acc cct ggc tcc aca   492
Tyr Leu Phe Ile Gln Thr Asp Lys Thr Ile Tyr Thr Pro Gly Ser Thr
        130   135   140

gtt ctc tat cgg atc ttc acc gtc aac cac aag ctg cta ccc gtg ggc   540
Val Leu Tyr Arg Ile Phe Thr Val Asn His Lys Leu Leu Pro Val Gly
145   150   155   160

cgg acg gtc atg gtc aac att gag aac ccg gaa ggc atc ccg gtc aag   588
Arg Thr Val Met Val Asn Ile Glu Asn Pro Glu Gly Ile Pro Val Lys
                165   170   175

cag gac tcc ttg tct tct cag aac cag ctt ggc gtc ttg ccc ttg tct   636
Gln Asp Ser Leu Ser Ser Gln Asn Gln Leu Gly Val Leu Pro Leu Ser
            180   185   190

tgg gac att ccg gaa ctc gtc aac atg ggc cag tgg aag atc cga gcc   684
Trp Asp Ile Pro Glu Leu Val Asn Met Gly Gln Trp Lys Ile Arg Ala
        195   200   205

tac tat gaa aac tca cca cag cag gtc ttc tcc act gag ttt gag gtg   732
Tyr Tyr Glu Asn Ser Pro Gln Gln Val Phe Ser Thr Glu Phe Glu Val
        210   215   220

aag gag tac gtg ctg ccc agt ttc gag gtc ata gtg gag cct aca gag   780
Lys Glu Tyr Val Leu Pro Ser Phe Glu Val Ile Val Glu Pro Thr Glu
225   230   235   240

aaa ttc tac tac atc tat aac gag aag ggc ctg gag gtc acc atc acc   828
Lys Phe Tyr Tyr Ile Tyr Asn Glu Lys Gly Leu Glu Val Thr Ile Thr
                245   250   255

gcc agg ttc ctc tac ggg aag aaa gtg gag gga act gcc ttt gtc atc   876
Ala Arg Phe Leu Tyr Gly Lys Lys Val Glu Gly Thr Ala Phe Val Ile
            260   265   270

ttc ggg atc cag gat ggc gaa cag agg att tcc ctg cct gaa tcc ctc   924
Phe Gly Ile Gln Asp Gly Glu Gln Arg Ile Ser Leu Pro Glu Ser Leu
        275   280   285

aag cgc att ccg att gag gat ggc tcg ggg gag gtt gtg ctg agc cgg   972
Lys Arg Ile Pro Ile Glu Asp Gly Ser Gly Glu Val Val Leu Ser Arg
        290   295   300

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aag gta ctg ctg gac ggg gtg cag aac ctc cga gca gaa gac ctg gtg    1020
Lys Val Leu Leu Asp Gly Val Gln Asn Leu Arg Ala Glu Asp Leu Val
305             310             315             320


ggg aag tct ttg tac gtg tct gcc acc gtc atc ttg cac tca ggc agt    1068
Gly Lys Ser Leu Tyr Val Ser Ala Thr Val Ile Leu His Ser Gly Ser
                325             330             335


gac atg gtg cag gca gag cgc agc ggg atc ccc atc gtg acc tct ccc    1116
Asp Met Val Gln Ala Glu Arg Ser Gly Ile Pro Ile Val Thr Ser Pro
            340             345             350


tac cag atc cac ttc acc aag aca ccc aag tac ttc aaa cca gga atg    1164
Tyr Gln Ile His Phe Thr Lys Thr Pro Lys Tyr Phe Lys Pro Gly Met
        355             360             365


ccc ttt gac ctc atg gtg ttc gtg acg aac cct gat ggc tct cca gcc    1212
Pro Phe Asp Leu Met Val Phe Val Thr Asn Pro Asp Gly Ser Pro Ala
    370             375             380


tac cga gtc ccc gtg gca gtc cag ggc gag gac act gtg cag tct cta    1260
Tyr Arg Val Pro Val Ala Val Gln Gly Glu Asp Thr Val Gln Ser Leu
385             390             395             400


acc cag gga gat ggc gtg gcc aaa ctc agc atc aac aca cac ccc agc    1308
Thr Gln Gly Asp Gly Val Ala Lys Leu Ser Ile Asn Thr His Pro Ser
                405             410             415


cag aag ccc ttg agc atc acg gtg cgc acg aag aag cag gag ctc tcg    1356
Gln Lys Pro Leu Ser Ile Thr Val Arg Thr Lys Lys Gln Glu Leu Ser
            420             425             430


gag gca gag cag gct acc agg acc atg cag gct ctg ccc tac agc acc    1404
Glu Ala Glu Gln Ala Thr Arg Thr Met Gln Ala Leu Pro Tyr Ser Thr
            435             440             445


gtg ggc aac tcc aac aat tac ctg cat ctc tca gtg cta cgt aca gag    1452
Val Gly Asn Ser Asn Asn Tyr Leu His Leu Ser Val Leu Arg Thr Glu
        450             455             460


ctc aga ccc ggg gag acc ctc aac gtc aac ttc ctc ctg cga atg gac    1500
Leu Arg Pro Gly Glu Thr Leu Asn Val Asn Phe Leu Leu Arg Met Asp
465             470             475             480
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cgc gcc cac gag gcc aag atc cgc tac tac acc tac ctg atc atg aac    1548
Arg Ala His Glu Ala Lys Ile Arg Tyr Tyr Thr Tyr Leu Ile Met Asn
            485                 490                 495


aag ggc agg ctg ttg aag gcg gga cgc cag gtg cga gag ccc ggc cag    1596
Lys Gly Arg Leu Leu Lys Ala Gly Arg Gln Val Arg Glu Pro Gly Gln
            500                 505                 510


gac ctg gtg gtg ctg ccc ctg tcc atc acc acc gac ttc atc cct tcc    1644
Asp Leu Val Val Leu Pro Leu Ser Ile Thr Thr Asp Phe Ile Pro Ser
            515                 520                 525


ttc cgc ctg gtg gcg tac tac acg ctg atc ggt gcc agc ggc cag agg    1692
Phe Arg Leu Val Ala Tyr Tyr Thr Leu Ile Gly Ala Ser Gly Gln Arg
            530                 535                 540


gag gtg gtg gcc gac tcc gtg tgg gtg gac gtc aag gac tcc tgc gtg    1740
Glu Val Val Ala Asp Ser Val Trp Val Asp Val Lys Asp Ser Cys Val
545                 550                 555                 560


ggc tcg ctg gtg gta aaa agc ggc cag tca gaa gac cgg cag cct gta    1788
Gly Ser Leu Val Val Lys Ser Gly Gln Ser Glu Asp Arg Gln Pro Val
            565                 570                 575


cct ggg cag cag atg acc ctg aag ata gag ggt gac cac ggg gcc cgg    1836
Pro Gly Gln Gln Met Thr Leu Lys Ile Glu Gly Asp His Gly Ala Arg
            580                 585                 590


gtg gta ctg gtg gcc gtg gac aag ggc gtg ttc gtg ctg aat aag aag    1884
Val Val Leu Val Ala Val Asp Lys Gly Val Phe Val Leu Asn Lys Lys
            595                 600                 605


aac aaa ctg acg cag agt aag atc tgg gac gtg gtg gag aag gca gac    1932
Asn Lys Leu Thr Gln Ser Lys Ile Trp Asp Val Val Glu Lys Ala Asp
            610                 615                 620


atc ggc tgc acc ccg ggc agt ggg aag gat tac gcc ggt gtc ttc tcc    1980
Ile Gly Cys Thr Pro Gly Ser Gly Lys Asp Tyr Ala Gly Val Phe Ser
625                 630                 635                 640


gac gca ggg ctg acc ttc acg agc agc agt ggc cag cag acc gcc cag    2028
Asp Ala Gly Leu Thr Phe Thr Ser Ser Ser Gly Gln Gln Thr Ala Gln
            645                 650                 655
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agg gca gaa ctt cag tgc ccg cag cca gcc gcc cgc cga cgc cgt tcc     2076
Arg Ala Glu Leu Gln Cys Pro Gln Pro Ala Ala Arg Arg Arg Arg Ser
            660                 665             670


gtg cag ctc acg gag aag cga atg gac aaa gtc ggc aag tac ccc aag     2124
Val Gln Leu Thr Glu Lys Arg Met Asp Lys Val Gly Lys Tyr Pro Lys
            675                 680             685


gag ctg cgc aag tgc tgc gag gac ggc atg cgg gag aac ccc atg agg     2172
Glu Leu Arg Lys Cys Cys Glu Asp Gly Met Arg Glu Asn Pro Met Arg
            690                 695             700


ttc tcg tgc cag cgc cgg acc cgt ttc atc tcc ctg ggc gag gcg tgc     2220
Phe Ser Cys Gln Arg Arg Thr Arg Phe Ile Ser Leu Gly Glu Ala Cys
705             710                 715                 720


aag aag gtc ttc ctg gac tgc tgc aac tac atc aca gag ctg cgg cgg     2268
Lys Lys Val Phe Leu Asp Cys Cys Asn Tyr Ile Thr Glu Leu Arg Arg
                725                 730             735


cag cac gcg cgg gcc agc cac ctg ggc ctg gcc agg agt aac ctg gat     2316
Gln His Ala Arg Ala Ser His Leu Gly Leu Ala Arg Ser Asn Leu Asp
                740             745             750


gag gac atc att gca gaa gag aac atc gtt tcc cga agt gag ttc cca     2364
Glu Asp Ile Ile Ala Glu Glu Asn Ile Val Ser Arg Ser Glu Phe Pro
            755                 760             765


gag agc tgg ctg tgg aac gtt gag gac ttg aaa gag cca ccg aaa aat     2412
Glu Ser Trp Leu Trp Asn Val Glu Asp Leu Lys Glu Pro Pro Lys Asn
            770             775             780


gga atc tct acg aag ctc atg aat ata ttt ttg aaa gac tcc atc acc     2460
Gly Ile Ser Thr Lys Leu Met Asn Ile Phe Leu Lys Asp Ser Ile Thr
785                 790                 795                 800


acg tgg gag att ctg gct gtc agc atg tcg gac aag aaa ggg atc tgt     2508
Thr Trp Glu Ile Leu Ala Val Ser Met Ser Asp Lys Lys Gly Ile Cys
                805                 810             815


gtg gca gac ccc ttc gag gtc aca gta atg cag gac ttc ttc atc gac     2556
Val Ala Asp Pro Phe Glu Val Thr Val Met Gln Asp Phe Phe Ile Asp
            820                 825             830
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ctg cgg cta ccc tac tct gtt gtt cga aac gag cag gtg gaa atc cga   2604
Leu Arg Leu Pro Tyr Ser Val Val Arg Asn Glu Gln Val Glu Ile Arg
        835   840   845

gcc gtt ctc tac aat tac cgg cag aac caa gag ctc aag gtg agg gtg   2652
Ala Val Leu Tyr Asn Tyr Arg Gln Asn Gln Glu Leu Lys Val Arg Val
        850   855   860

gaa cta ctc cac aat cca gcc ttc tgc agc ctg gcc acc acc aag agg   2700
Glu Leu Leu His Asn Pro Ala Phe Cys Ser Leu Ala Thr Thr Lys Arg
865   870   875   880

cgt cac cag cag acc gta acc atc ccc ccc aag tcc tcg ttg tcc gtt   2748
Arg His Gln Gln Thr Val Thr Ile Pro Pro Lys Ser Ser Leu Ser Val
            885   890   895

cca tat gtc atc gtg ccg cta aag acc ggc ctg cag gaa gtg gaa gtc   2796
Pro Tyr Val Ile Val Pro Leu Lys Thr Gly Leu Gln Glu Val Glu Val
            900   905   910

aag gct gcc gtc tac cat cat ttc atc agt gac ggt gtc agg aag tcc   2844
Lys Ala Ala Val Tyr His His Phe Ile Ser Asp Gly Val Arg Lys Ser
        915   920   925

ctg aag gtc gtg ccg gaa gga atc aga atg aac aaa act gtg gct gtt   2892
Leu Lys Val Val Pro Glu Gly Ile Arg Met Asn Lys Thr Val Ala Val
        930   935   940

cgc acc ctg gat cca gaa cgc ctg ggc cgt gaa gga gtg cag aaa gag   2940
Arg Thr Leu Asp Pro Glu Arg Leu Gly Arg Glu Gly Val Gln Lys Glu
945   950   955   960

gac atc cca cct gca gac ctc agt gac caa gtc ccg gac acc gag tct   2988
Asp Ile Pro Pro Ala Asp Leu Ser Asp Gln Val Pro Asp Thr Glu Ser
            965   970   975

gag acc aga att ctc ctg caa ggg acc cca gtg gcc cag atg aca gag   3036
Glu Thr Arg Ile Leu Leu Gln Gly Thr Pro Val Ala Gln Met Thr Glu
            980   985   990

gat gcc gtc gac gcg gaa cgg ctg aag cac ctc att gtg acc ccc tcg   3084
Asp Ala Val Asp Ala Glu Arg Leu Lys His Leu Ile Val Thr Pro Ser
        995   1000   1005

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ggc tgc ggg gaa cag aac atg atc ggc atg acg ccc acg gtc atc gct        3132
Gly Cys Gly Glu Gln Asn Met Ile Gly Met Thr Pro Thr Val Ile Ala
    1010             1015             1020


gtg cat tac ctg gat gaa acg gag cag tgg gag aag ttc ggc cta gag        3180
Val His Tyr Leu Asp Glu Thr Glu Gln Trp Glu Lys Phe Gly Leu Glu
1025             1030             1035             1040


aag cgg cag ggg gcc ttg gag ctc atc aag aag ggg tac acc cag cag        3228
Lys Arg Gln Gly Ala Leu Glu Leu Ile Lys Lys Gly Tyr Thr Gln Gln
                1045             1050             1055


ctg gcc ttc aga caa ccc agc tct gcc ttt gcg gcc ttc gtg aaa cgg        3276
Leu Ala Phe Arg Gln Pro Ser Ser Ala Phe Ala Ala Phe Val Lys Arg
                1060             1065             1070


gca ccc agc acc tgg ctg acc gcc tac gtg gtc aag gtc ttc tct ctg        3324
Ala Pro Ser Thr Trp Leu Thr Ala Tyr Val Val Lys Val Phe Ser Leu
        1075             1080             1085


gct gtc aac ctc atc gcc atc gac tcc caa gtc ctc tgc ggg gct gtt        3372
Ala Val Asn Leu Ile Ala Ile Asp Ser Gln Val Leu Cys Gly Ala Val
        1090             1095             1100


aaa tgg ctg atc ctg gag aag cag aag ccc gac ggg gtc ttc cag gag        3420
Lys Trp Leu Ile Leu Glu Lys Gln Lys Pro Asp Gly Val Phe Gln Glu
1105             1110             1115             1120


gat gcg ccc gtg ata cac caa gaa atg att ggt gga tta cgg aac aac        3468
Asp Ala Pro Val Ile His Gln Glu Met Ile Gly Gly Leu Arg Asn Asn
                1125             1130             1135


aac gag aaa gac atg gcc ctc acg gcc ttt gtt ctc atc tcg ctg cag        3516
Asn Glu Lys Asp Met Ala Leu Thr Ala Phe Val Leu Ile Ser Leu Gln
            1140             1145             1150


gag gct aaa gat att tgc gag gag cag gtc aac agc ctg cca ggc agc        3564
Glu Ala Lys Asp Ile Cys Glu Glu Gln Val Asn Ser Leu Pro Gly Ser
        1155             1160             1165


atc act aaa gca gga gac ttc ctt gaa gcc aac tac atg aac cta cag        3612
Ile Thr Lys Ala Gly Asp Phe Leu Glu Ala Asn Tyr Met Asn Leu Gln
    1170             1175             1180
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aga tcc tac act gtg gcc att gct ggc tat gct ctg gcc cag atg ggc    3660
Arg Ser Tyr Thr Val Ala Ile Ala Gly Tyr Ala Leu Ala Gln Met Gly
1185                1190                1195                1200


agg ctg aag ggg cct ctt ctt aac aaa ttt ctg acc aca gcc aaa gat    3708
Arg Leu Lys Gly Pro Leu Leu Asn Lys Phe Leu Thr Thr Ala Lys Asp
                    1205                1210                1215


aag aac cgc tgg gag gac cct ggt aag cag ctc tac aac gtg gag gcc    3756
Lys Asn Arg Trp Glu Asp Pro Gly Lys Gln Leu Tyr Asn Val Glu Ala
                1220                1225                1230


aca tcc tat gcc ctc ttg gcc cta ctg cag cta aaa gac ttt gac ttt    3804
Thr Ser Tyr Ala Leu Leu Ala Leu Leu Gln Leu Lys Asp Phe Asp Phe
            1235                1240                1245


gtg cct ccc gtc gtg cgt tgg ctc aat gaa cag aga tac tac ggt ggt    3852
Val Pro Pro Val Val Arg Trp Leu Asn Glu Gln Arg Tyr Tyr Gly Gly
        1250                1255                1260


ggc tat ggc tct acc cag gcc acc ttc atg gtg ttc caa gcc ttg gct    3900
Gly Tyr Gly Ser Thr Gln Ala Thr Phe Met Val Phe Gln Ala Leu Ala
1265                1270                1275                1280


caa tac caa aag gac gcc cct gac cac cag gaa ctg aac ctt gat gtg    3948
Gln Tyr Gln Lys Asp Ala Pro Asp His Gln Glu Leu Asn Leu Asp Val
                    1285                1290                1295


tcc ctc caa ctg ccc agc cgc agc tcc aag atc acc cac cgt atc cac    3996
Ser Leu Gln Leu Pro Ser Arg Ser Ser Lys Ile Thr His Arg Ile His
                1300                1305                1310


tgg gaa tct gcc agc ctc ctg cga tca gaa gag acc aag gaa aat gag    4044
Trp Glu Ser Ala Ser Leu Leu Arg Ser Glu Glu Thr Lys Glu Asn Glu
            1315                1320                1325


ggt ttc aca gtc aca gct gaa gga aaa ggc caa ggc acc ttg tcg gtg    4092
Gly Phe Thr Val Thr Ala Glu Gly Lys Gly Gln Gly Thr Leu Ser Val
        1330                1335                1340


gtg aca atg tac cat gct aag gcc aaa gat caa ctc acc tgt aat aaa    4140
Val Thr Met Tyr His Ala Lys Ala Lys Asp Gln Leu Thr Cys Asn Lys
1345                1350                1355                1360
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ttc gac ctc aag gtc acc ata aaa cca gca ccg gaa aca gaa aag agg    4188
Phe Asp Leu Lys Val Thr Ile Lys Pro Ala Pro Glu Thr Glu Lys Arg
            1365             1370             1375

cct cag gat gcc aag aac act atg atc ctt gag atc tgt acc agg tac    4236
Pro Gln Asp Ala Lys Asn Thr Met Ile Leu Glu Ile Cys Thr Arg Tyr
            1380             1385             1390

cgg gga gac cag gat gcc act atg tct ata ttg gac ata tcc atg atg    4284
Arg Gly Asp Gln Asp Ala Thr Met Ser Ile Leu Asp Ile Ser Met Met
            1395             1400             1405

act ggc ttt gct cca gac aca gat gac ctg aag cag ctg gcc aat ggt    4332
Thr Gly Phe Ala Pro Asp Thr Asp Asp Leu Lys Gln Leu Ala Asn Gly
         1410             1415             1420

gtt gac aga tac atc tcc aag tat gag ctg gac aaa gcc ttc tcc gat    4380
Val Asp Arg Tyr Ile Ser Lys Tyr Glu Leu Asp Lys Ala Phe Ser Asp
1425             1430             1435             1440

agg aac acc ctc atc atc tac ctg gac aag gtc tca cac tct gag gat    4428
Arg Asn Thr Leu Ile Ile Tyr Leu Asp Lys Val Ser His Ser Glu Asp
            1445             1450             1455

gac tgt cta gct ttc aaa gtt cac caa tac ttt aat gta gag ctt atc    4476
Asp Cys Leu Ala Phe Lys Val His Gln Tyr Phe Asn Val Glu Leu Ile
            1460             1465             1470

cag cct gga gca gtc aag gtc tac gcc tat tac aac ctg gag gaa agc    4524
Gln Pro Gly Ala Val Lys Val Tyr Ala Tyr Tyr Asn Leu Glu Glu Ser
            1475             1480             1485

tgt acc cgg ttc tac cat ccg gaa aag gag gat gga aag ctg aac aag    4572
Cys Thr Arg Phe Tyr His Pro Glu Lys Glu Asp Gly Lys Leu Asn Lys
         1490             1495             1500

ctc tgc cgt gat gaa ctg tgc cgc tgt gct gag gag aat tgc ttc ata    4620
Leu Cys Arg Asp Glu Leu Cys Arg Cys Ala Glu Glu Asn Cys Phe Ile
1505             1510             1515             1520

caa aag tcg gat gac aag gtc acc ctg gaa gaa cgg ctg gac aag gcc    4668
Gln Lys Ser Asp Asp Lys Val Thr Leu Glu Glu Arg Leu Asp Lys Ala
            1525             1530             1535
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tgt gag cca gga gtg gac tat gtg tac aag acc cga ctg gtc aag gtt     4716
Cys Glu Pro Gly Val Asp Tyr Val Tyr Lys Thr Arg Leu Val Lys Val
        1540                1545                1550


cag ctg tcc aat gac ttt gac gag tac atc atg gcc att gag cag acc     4764
Gln Leu Ser Asn Asp Phe Asp Glu Tyr Ile Met Ala Ile Glu Gln Thr
        1555                1560                1565


atc aag tca ggc tcg gat gag gtg cag gtt gga cag cag cgc acg ttc     4812
Ile Lys Ser Gly Ser Asp Glu Val Gln Val Gly Gln Gln Arg Thr Phe
        1570                1575                1580


atc agc ccc atc aag tgc aga gaa gcc ctg aag ctg gag gag aag aaa     4860
Ile Ser Pro Ile Lys Cys Arg Glu Ala Leu Lys Leu Glu Glu Lys Lys
1585                1590                1595                1600


cac tac ctc atg tgg ggt ctc tcc tcc gat ttc tgg gga gag aag ccc     4908
His Tyr Leu Met Trp Gly Leu Ser Ser Asp Phe Trp Gly Glu Lys Pro
                1605                1610                1615


aac ctc agc tac atc atc ggg aag gac act tgg gtg gag cac tgg cct     4956
Asn Leu Ser Tyr Ile Ile Gly Lys Asp Thr Trp Val Glu His Trp Pro
                1620                1625                1630


gag gag gac gaa tgc caa gac gaa gag aac cag aaa caa tgc cag gac     5004
Glu Glu Asp Glu Cys Gln Asp Glu Glu Asn Gln Lys Gln Cys Gln Asp
        1635                1640                1645


ctc ggc gcc ttc acc gag agc atg gtt gtc ttt ggg tgc ccc aac tga     5052
Leu Gly Ala Phe Thr Glu Ser Met Val Val Phe Gly Cys Pro Asn
        1650                1655                1660


ccacacccc attcc                                                      5067
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<223> PCR Primer

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<223> PCR Probe

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cctgcccctt accccttcat tccttccacc tttttccttc actatgggac cagcttcagg   180

gtcccagcta ctagtgctac tgctgctgtt ggccagctcc ccattagctc tggggatccc   240

catgtaagta gttacctttt gggggtgcag tttcttatac aatttaggag tcacctaggt   300

gagtcaccta ggagtcaccc acttggggggg agacagggat gttaagaatt tgtgctggggg   360

gctggaggat ggctcagtgg gtatgaagtc ttgctgcatg gacataagga ccttaactca   420

aactcccagc acccacagaa aagccaggag tggcctccag agcctgtaac cccacactgt   480

ggggctggag accagatact ggggcttgct gactgccagc ccagtgccag gttcagagag   540

agatgttgac tcaaggtgtg gggagggagg ggcatagaac aggacaccgg acatcttcct   600

gtgacgtgac atacatacat acatacatac atacatac atacatac aaacagagag   660

aaagagagag aatgtgagtg tttgggttgt cttatgttca tagaactcag gtattgtagc   720

attggtgtgc ctacttatga agaagaaggt ctatagattt atggtgtctg tgatgtcttg   780

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<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 80
taccagggtc ctcccagcgg   20

<210> 81
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<220>

<223> Antisense Oligonucleotide

<400> 81
gcataggatg tggcctccac   20

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<223> Antisense Oligonucleotide

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tggaacacca tgaaggtggc                                        20


<210> 83
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<223> Antisense Oligonucleotide

<400> 83
gtattgagcc aaggcttgga                                        20


<210> 84
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<220>

<223> Antisense Oligonucleotide

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ggtgatcttg gagctgcggc                                        20


<210> 85
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gttcttggca tcctgaggcc   20

<210> 86
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<220>

<223> Antisense Oligonucleotide

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gcaaagccag tcatcatgga   20

<210> 87
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<220>

<223> Antisense Oligonucleotide

<400> 87
ctggagcaaa gccagtcatc   20

<210> 88
<211> 20
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<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 88
tgtgtctgga gcaaagccag   20

<210> 89
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 89
gaaggctttg tccagctcat   20

<210> 90
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<212> DNA
<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 90
ggtagatgat gagggtgttc   20

<210> 91
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<212> DNA
<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 91
ctcagagtgt gagaccttgt   20

<210> 92
<211> 20
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<220>

<223> Antisense Oligonucleotide

<400> 92
ccttttccgg atggtagaac   20

<210> 93
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<212> DNA
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<220>

<223> Antisense Oligonucleotide

<400> 93
gtactcgtca aagtcattgg   20

<210> 94
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<220>

<223> Antisense Oligonucleotide

<400> 94
ccacatgagg tagtgtttct   20

<210> 95
<211> 20
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<220>

<223> Antisense Oligonucleotide

<400> 95
tcggaggaga gaccccacat   20

<210> 96
<211> 20
<212> DNA
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<220>

<223> Antisense Oligonucleotide

<400> 96
tcaggccagt gctccaccca   20

<210> 97
<211> 20
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<220>

<223> Antisense Oligonucleotide

<400> 97
ggcatcacac acgaagccca   20

<210> 98
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 98

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tgcggcagcc gctgcccatg                                             20
```

```
<210> 99
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 99
gtcatagctg tggcagcctg                                             20
```

```
<210> 100
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 100
ggttgagctc cacatctgcc                                             20
```

```
<210> 101
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 101
ttgaagaaat cctccttgtc                                             20
```

```
<210> 102
<211> 20
```

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 102

atgcattcga tgcggcagcc   20

<210> 103

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 103

caaacagctc tcgggagatg   20

<210> 104

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 104

tagctcatgc ctgtcttgca   20

<210> 105

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 105
ggagggacta cccacagcaa   20

<210> 106
<211> 20
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<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 106
actcgctgaa gaatatgcat   20

<210> 107
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 107
catcatactc ctgggccacc   20

<210> 108
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 108
aacttctgct tgctctcctc   20

<210> 109
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 109
tgggcaccaa cttctgcttg   20

<210> 110
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 110
tctgcttgct ctcctccatg   20

<210> 111
<211> 5087
<212> DNA
<213> Mus musculus

<220>

<220>
<221> CDS
<222> (57)...(5048)

<400> 111
gcctctgccc acccctgccc cttacccctt cattccttcc accttttcc ttcact atg   59
                                                                Met
                                                                1

gga cca gct tca ggg tcc cag cta cta gtg cta ctg ctg ctg ttg gcc   107

```
                Gly Pro Ala Ser Gly Ser Gln Leu Leu Val Leu Leu Leu Leu Ala
                            5               10              15
```

```
agc tcc cca tta gct ctg ggg atc ccc atg tat tcc atc att act ccc        155
Ser Ser Pro Leu Ala Leu Gly Ile Pro Met Tyr Ser Ile Ile Thr Pro
            20              25              30
```

```
aat gtc cta cgg ctg gag agc gaa gag acc atc gta ctg gag gcc cac        203
Asn Val Leu Arg Leu Glu Ser Glu Glu Thr Ile Val Leu Glu Ala His
        35              40              45
```

```
gat gct cag ggt gac atc cca gtc aca gtc act gtg caa gac ttc cta        251
Asp Ala Gln Gly Asp Ile Pro Val Thr Val Thr Val Gln Asp Phe Leu
50              55              60              65
```

```
aag agg caa gtg ctg acc agt gag aag aca gtg ttg aca gga gcc agt        299
Lys Arg Gln Val Leu Thr Ser Glu Lys Thr Val Leu Thr Gly Ala Ser
                70              75              80
```

```
gga cat ctg aga agc gtc tcc atc aag att cca gcc agt aag gaa ttc        347
Gly His Leu Arg Ser Val Ser Ile Lys Ile Pro Ala Ser Lys Glu Phe
            85              90              95
```

```
aac tca gat aag gag ggg cac aag tac gtg aca gtg gtg gca aac ttc        395
Asn Ser Asp Lys Glu Gly His Lys Tyr Val Thr Val Val Ala Asn Phe
            100             105             110
```

```
ggg gaa acg gtg gtg gag aaa gca gtg atg gta agc ttc cag agt ggg        443
Gly Glu Thr Val Val Glu Lys Ala Val Met Val Ser Phe Gln Ser Gly
    115             120             125
```

```
tac ctc ttc atc cag aca gac aag acc atc tac acc cct ggc tcc act        491
Tyr Leu Phe Ile Gln Thr Asp Lys Thr Ile Tyr Thr Pro Gly Ser Thr
130             135             140             145
```

```
gtc tta tat cgg atc ttc act gtg gac aac aac cta ctg ccc gtg ggc        539
Val Leu Tyr Arg Ile Phe Thr Val Asp Asn Asn Leu Leu Pro Val Gly
            150             155             160
```

```
aag aca gtc gtc atc ctc att gag acc ccc gat ggc att cct gtc aag        587
Lys Thr Val Val Ile Leu Ile Glu Thr Pro Asp Gly Ile Pro Val Lys
            165             170             175
```

```
aga gac att ctg tct tcc aac aac caa cac ggc atc ttg cct ttg tct        635
```

```
Arg Asp Ile Leu Ser Ser Asn Asn Gln His Gly Ile Leu Pro Leu Ser
        180                 185                 190


tgg aac att cct gaa ctg gtc aac atg ggg cag tgg aag atc cga gcc    683
Trp Asn Ile Pro Glu Leu Val Asn Met Gly Gln Trp Lys Ile Arg Ala
        195                 200                 205


ttt tac gaa cat gcg ccg aag cag atc ttc tcc gca gag ttt gag gtg    731
Phe Tyr Glu His Ala Pro Lys Gln Ile Phe Ser Ala Glu Phe Glu Val
210                 215                 220                 225


aag gaa tac gtg ctg ccc agt ttt gag gtc cgg gtg gag ccc aca gag    779
Lys Glu Tyr Val Leu Pro Ser Phe Glu Val Arg Val Glu Pro Thr Glu
                230                 235                 240


aca ttt tat tac atc gat gac cca aat ggc ctg gaa gtt tcc atc ata    827
Thr Phe Tyr Tyr Ile Asp Asp Pro Asn Gly Leu Glu Val Ser Ile Ile
            245                 250                 255


gcc aag ttc ctg tac ggg aaa aac gtg gac ggg aca gcc ttc gtg att    875
Ala Lys Phe Leu Tyr Gly Lys Asn Val Asp Gly Thr Ala Phe Val Ile
        260                 265                 270


ttt ggg gtc cag gat ggc gat aag aag att tct ctg gcc cac tcc ctc    923
Phe Gly Val Gln Asp Gly Asp Lys Lys Ile Ser Leu Ala His Ser Leu
        275                 280                 285


acg cgc gta gtg att gag gat ggt gtg ggg gat gca gtg ctg acc cgg    971
Thr Arg Val Val Ile Glu Asp Gly Val Gly Asp Ala Val Leu Thr Arg
290                 295                 300                 305


aag gtg ctg atg gag ggg gta cgg cct tcc aac gcc gac gcc ctg gtg   1019
Lys Val Leu Met Glu Gly Val Arg Pro Ser Asn Ala Asp Ala Leu Val
                310                 315                 320


ggg aag tcc ctg tat gtc tcc gtc act gtc atc ctg cac tca ggt agt   1067
Gly Lys Ser Leu Tyr Val Ser Val Thr Val Ile Leu His Ser Gly Ser
            325                 330                 335


gac atg gta gag gca gag cgc agt ggg atc ccg att gtc act tcc ccg   1115
Asp Met Val Glu Ala Glu Arg Ser Gly Ile Pro Ile Val Thr Ser Pro
            340                 345                 350


tac cag atc cac ttc acc aag aca ccc aaa ttc ttc aag cca gcc atg   1163
```

Tyr Gln Ile His Phe Thr Lys Thr Pro Lys Phe Phe Lys Pro Ala Met
    355   360   365

ccc ttt gac ctc atg gtg ttc gtg acc aac ccc gat ggc tct ccg gcc   1211
Pro Phe Asp Leu Met Val Phe Val Thr Asn Pro Asp Gly Ser Pro Ala
370   375   380   385

agc aaa gtg ctg gtg gtc act cag gga tct aat gca aag gct ctc acc   1259
Ser Lys Val Leu Val Val Thr Gln Gly Ser Asn Ala Lys Ala Leu Thr
            390   395   400

caa gat gat ggc gtg gcc aag cta agc atc aac aca ccc aac agc cgc   1307
Gln Asp Asp Gly Val Ala Lys Leu Ser Ile Asn Thr Pro Asn Ser Arg
            405   410   415

caa ccc ctg acc atc aca gtc cgc acc aag aag gac act ctc cca gaa   1355
Gln Pro Leu Thr Ile Thr Val Arg Thr Lys Lys Asp Thr Leu Pro Glu
        420   425   430

tca cgg cag gcc acc aag aca atg gag gcc cat ccc tac agc act atg   1403
Ser Arg Gln Ala Thr Lys Thr Met Glu Ala His Pro Tyr Ser Thr Met
        435   440   445

cac aac tcc aac aac tac cta cac ttg tca gtg tca cga atg gag ctc   1451
His Asn Ser Asn Asn Tyr Leu His Leu Ser Val Ser Arg Met Glu Leu
450   455   460   465

aag ccg ggg gac aac ctc aat gtc aac ttc cac ctg cgc aca gac cca   1499
Lys Pro Gly Asp Asn Leu Asn Val Asn Phe His Leu Arg Thr Asp Pro
            470   475   480

ggc cat gag gcc aag atc cga tac tac acc tac ctg gtt atg aac aag   1547
Gly His Glu Ala Lys Ile Arg Tyr Tyr Thr Tyr Leu Val Met Asn Lys
            485   490   495

ggg aag ctc ctg aag gca ggc cgc cag gtt cgg gag cct ggc cag gac   1595
Gly Lys Leu Leu Lys Ala Gly Arg Gln Val Arg Glu Pro Gly Gln Asp
        500   505   510

ctg gtg gtc ttg tcc ctg ccc atc act cca gag ttt att cct tca ttt   1643
Leu Val Val Leu Ser Leu Pro Ile Thr Pro Glu Phe Ile Pro Ser Phe
        515   520   525

cgc ctg gtg gct tac tac acc ctg att gga gct agt ggc cag agg gag   1691

```
Arg Leu Val Ala Tyr Tyr Thr Leu Ile Gly Ala Ser Gly Gln Arg Glu
530             535             540             545


gtg gtg gct gac tct gtg tgg gtg gat gtg aag gat tcc tgt att ggc    1739
Val Val Ala Asp Ser Val Trp Val Asp Val Lys Asp Ser Cys Ile Gly
                550                 555             560


acg ctg gtg gtg aag ggt gac cca aga gat aac cat ctc gca cct ggg    1787
Thr Leu Val Val Lys Gly Asp Pro Arg Asp Asn His Leu Ala Pro Gly
            565                 570             575


caa caa acg aca ctc agg att gaa gga aac cag ggg gcc cga gtg ggg    1835
Gln Gln Thr Thr Leu Arg Ile Glu Gly Asn Gln Gly Ala Arg Val Gly
        580                 585             590


cta gtg gct gtg gac aag gga gtg ttt gtg ctg aac aag aag aac aaa    1883
Leu Val Ala Val Asp Lys Gly Val Phe Val Leu Asn Lys Lys Asn Lys
        595                 600             605


ctc aca cag agc aag atc tgg gat gtg gta gag aag gca gac att ggc    1931
Leu Thr Gln Ser Lys Ile Trp Asp Val Val Glu Lys Ala Asp Ile Gly
610             615             620             625


tgc acc cca ggc agt ggg aag aac tat gct ggt gtc ttc atg gat gca    1979
Cys Thr Pro Gly Ser Gly Lys Asn Tyr Ala Gly Val Phe Met Asp Ala
                630                 635             640


ggc ctg gcc ttc aag aca agc caa gga ctg cag act gaa cag aga gca    2027
Gly Leu Ala Phe Lys Thr Ser Gln Gly Leu Gln Thr Glu Gln Arg Ala
            645                 650             655


gat ctt gag tgc acc aag cca gca gcc cgc cgc cgt cgc tca gta cag    2075
Asp Leu Glu Cys Thr Lys Pro Ala Ala Arg Arg Arg Arg Ser Val Gln
            660                 665             670


ttg atg gaa aga agg atg gac aaa gct ggt cag tac act gac aag ggt    2123
Leu Met Glu Arg Arg Met Asp Lys Ala Gly Gln Tyr Thr Asp Lys Gly
        675                 680             685


ctt cgg aag tgt tgt gag gat ggt atg cgg gat atc cct atg aga tac    2171
Leu Arg Lys Cys Cys Glu Asp Gly Met Arg Asp Ile Pro Met Arg Tyr
690             695             700             705


agc tgc cag cgc cgg gca cgc ctc atc acc cag ggc gag aac tgc ata    2219
```

```
                Ser Cys Gln Arg Arg Ala Arg Leu Ile Thr Gln Gly Glu Asn Cys Ile
                          710                 715                 720


aag gcc ttc ata gac tgc tgc aac cac atc acc aag ctg cgt gaa caa         2267
Lys Ala Phe Ile Asp Cys Cys Asn His Ile Thr Lys Leu Arg Glu Gln
              725                 730                 735


cac aga aga gac cac gtg ctg ggc ctg gcc agg agt gaa ttg gag gaa         2315
His Arg Arg Asp His Val Leu Gly Leu Ala Arg Ser Glu Leu Glu Glu
          740                 745                 750


gac ata att cca gaa gaa gat att atc tct aga agc cac ttc cca cag         2363
Asp Ile Ile Pro Glu Glu Asp Ile Ile Ser Arg Ser His Phe Pro Gln
          755                 760                 765


agc tgg ttg tgg acc ata gaa gag ttg aaa gaa cca gag aaa aat gga         2411
Ser Trp Leu Trp Thr Ile Glu Glu Leu Lys Glu Pro Glu Lys Asn Gly
770                 775                 780                 785


atc tct acg aag gtc atg aac atc ttt ctc aaa gat tcc atc acc acc         2459
Ile Ser Thr Lys Val Met Asn Ile Phe Leu Lys Asp Ser Ile Thr Thr
              790                 795                 800


tgg gag att ctg gca gtg agc ttg tca gac aag aaa ggg atc tgt gtg         2507
Trp Glu Ile Leu Ala Val Ser Leu Ser Asp Lys Lys Gly Ile Cys Val
              805                 810                 815


gca gac ccc tat gag atc aga gtg atg cag gac ttc ttc att gac ctg         2555
Ala Asp Pro Tyr Glu Ile Arg Val Met Gln Asp Phe Phe Ile Asp Leu
          820                 825                 830


cgg ctg ccc tac tct gta gtg cgc aac gaa cag gtg gag atc aga gct         2603
Arg Leu Pro Tyr Ser Val Val Arg Asn Glu Gln Val Glu Ile Arg Ala
          835                 840                 845


gtg ctc ttc aac tac cgt gaa cag cag gaa ctt aag gtg agg gtg gaa         2651
Val Leu Phe Asn Tyr Arg Glu Gln Gln Glu Leu Lys Val Arg Val Glu
850                 855                 860                 865


ctg ttg cat aat cca gcc ttc tgc agc atg gcc acc gcc aag aat cgc         2699
Leu Leu His Asn Pro Ala Phe Cys Ser Met Ala Thr Ala Lys Asn Arg
              870                 875                 880


tac ttc cag acc atc aaa atc cct ccc aag tcc tcg gtg gct gta ccg         2747
```

```
         Tyr Phe Gln Thr Ile Lys Ile Pro Pro Lys Ser Ser Val Ala Val Pro
                     885             890             895
```

```
tat gtc att gtc ccc ttg aag atc ggc caa caa gag gtg gag gtc aag        2795
Tyr Val Ile Val Pro Leu Lys Ile Gly Gln Gln Glu Val Glu Val Lys
        900             905             910
```

```
gct gct gtc ttc aat cac ttc atc agt gat ggt gtc aag aag aca ctg        2843
Ala Ala Val Phe Asn His Phe Ile Ser Asp Gly Val Lys Lys Thr Leu
        915             920             925
```

```
aag gtc gtg cca gaa gga atg aga atc aac aaa act gtg gcc atc cat        2891
Lys Val Val Pro Glu Gly Met Arg Ile Asn Lys Thr Val Ala Ile His
930             935             940             945
```

```
aca ctg gac cca gag aag ctc ggt caa ggg gga gtg cag aag gtg gat        2939
Thr Leu Asp Pro Glu Lys Leu Gly Gln Gly Gly Val Gln Lys Val Asp
                950             955             960
```

```
gtg cct gcc gca gac ctt agc gac caa gtg cca gac aca gac tct gag        2987
Val Pro Ala Ala Asp Leu Ser Asp Gln Val Pro Asp Thr Asp Ser Glu
            965             970             975
```

```
acc aga att atc ctg caa ggg agc ccg gtg gtt cag atg gct gaa gat        3035
Thr Arg Ile Ile Leu Gln Gly Ser Pro Val Val Gln Met Ala Glu Asp
        980             985             990
```

```
gct gtg gac ggg gag cgg ctg aaa cac ctg atc gtg acc ccc gca ggc        3083
Ala Val Asp Gly Glu Arg Leu Lys His Leu Ile Val Thr Pro Ala Gly
    995             1000            1005
```

```
tgt ggg gaa cag aac atg att ggc atg aca cca aca gtc att gcg gta        3131
Cys Gly Glu Gln Asn Met Ile Gly Met Thr Pro Thr Val Ile Ala Val
1010            1015            1020            1025
```

```
cac tac ctg gac cag acc gaa cag tgg gag aag ttc ggc ata gag aag        3179
His Tyr Leu Asp Gln Thr Glu Gln Trp Glu Lys Phe Gly Ile Glu Lys
                1030            1035            1040
```

```
agg caa gag gcc ctg gag ctc atc aag aaa ggg tac acc cag cag ctg        3227
Arg Gln Glu Ala Leu Glu Leu Ile Lys Lys Gly Tyr Thr Gln Gln Leu
            1045            1050            1055
```

```
gcc ttc aaa cag ccc agc tct gcc tat gct gcc ttc aac aac cgg ccc        3275
```

```
Ala Phe Lys Gln Pro Ser Ser Ala Tyr Ala Ala Phe Asn Asn Arg Pro
        1060                1065                1070


ccc agc acc tgg ctg aca gcc tac gtg gtc aag gtc ttc tct cta gct     3323
Pro Ser Thr Trp Leu Thr Ala Tyr Val Val Lys Val Phe Ser Leu Ala
        1075                1080                1085


gcc aac ctc atc gcc atc gac tct cac gtc ctg tgt ggg gct gtt aaa     3371
Ala Asn Leu Ile Ala Ile Asp Ser His Val Leu Cys Gly Ala Val Lys
1090                1095                1100                1105


tgg ttg att ctg gag aaa cag aag ccg gat ggt gtc ttt cag gag gat     3419
Trp Leu Ile Leu Glu Lys Gln Lys Pro Asp Gly Val Phe Gln Glu Asp
                1110                1115                1120


ggg ccc gtg att cac caa gaa atg att ggt ggc ttc cgg aac gcc aag     3467
Gly Pro Val Ile His Gln Glu Met Ile Gly Gly Phe Arg Asn Ala Lys
            1125                1130                1135


gag gca gat gtg tca ctc aca gcc ttc gtc ctc atc gca ctg cag gaa     3515
Glu Ala Asp Val Ser Leu Thr Ala Phe Val Leu Ile Ala Leu Gln Glu
        1140                1145                1150


gcc agg gac atc tgt gag ggg cag gtc aat agc ctt cct ggg agc atc     3563
Ala Arg Asp Ile Cys Glu Gly Gln Val Asn Ser Leu Pro Gly Ser Ile
        1155                1160                1165


aac aag gca ggg gag tat att gaa gcc agt tac atg aac ctg cag aga     3611
Asn Lys Ala Gly Glu Tyr Ile Glu Ala Ser Tyr Met Asn Leu Gln Arg
1170                1175                1180                1185


cca tac aca gtg gcc att gct ggg tat gcc ctg gcc ctg atg aac aaa     3659
Pro Tyr Thr Val Ala Ile Ala Gly Tyr Ala Leu Ala Leu Met Asn Lys
                1190                1195                1200


ctg gag gaa cct tac ctc ggc aag ttt ctg aac aca gcc aaa gat cgg     3707
Leu Glu Glu Pro Tyr Leu Gly Lys Phe Leu Asn Thr Ala Lys Asp Arg
            1205                1210                1215


aac cgc tgg gag gag cct gac cag cag ctc tac aac gta gag gcc aca     3755
Asn Arg Trp Glu Glu Pro Asp Gln Gln Leu Tyr Asn Val Glu Ala Thr
            1220                1225                1230


tcc tac gcc ctc ctg gcc ctg ctg ctg ctg aaa gac ttt gac tct gtg     3803
```

```
Ser Tyr Ala Leu Leu Ala Leu Leu Leu Leu Lys Asp Phe Asp Ser Val
    1235             1240             1245


ccc cct gta gtg cgc tgg ctc aat gag caa aga tac tac gga ggc ggc   3851
Pro Pro Val Val Arg Trp Leu Asn Glu Gln Arg Tyr Tyr Gly Gly Gly
1250             1255             1260             1265


tat ggc tcc acc cag gct acc ttc atg gta ttc caa gcc ttg gcc caa   3899
Tyr Gly Ser Thr Gln Ala Thr Phe Met Val Phe Gln Ala Leu Ala Gln
                1270             1275             1280


tat caa aca gat gtc cct gac cat aag gac ttg aac atg gat gtg tcc   3947
Tyr Gln Thr Asp Val Pro Asp His Lys Asp Leu Asn Met Asp Val Ser
            1285             1290             1295


ttc cac ctc ccc agc cgt agc tct gca acc acg ttt cgc ctg ctc tgg   3995
Phe His Leu Pro Ser Arg Ser Ser Ala Thr Thr Phe Arg Leu Leu Trp
        1300             1305             1310


gaa aat ggc aac ctc ctg cga tcg gaa gag acc aag caa aat gag gcc   4043
Glu Asn Gly Asn Leu Leu Arg Ser Glu Glu Thr Lys Gln Asn Glu Ala
        1315             1320             1325


ttc tct cta aca gcc aaa gga aaa ggc cga ggc aca ttg tcg gtg gtg   4091
Phe Ser Leu Thr Ala Lys Gly Lys Gly Arg Gly Thr Leu Ser Val Val
1330             1335             1340             1345


gca gtg tat cat gcc aaa ctc aaa agc aaa gtc acc tgc aag aag ttt   4139
Ala Val Tyr His Ala Lys Leu Lys Ser Lys Val Thr Cys Lys Lys Phe
                1350             1355             1360


gac ctc agg gtc agc ata aga cca gcc cct gag aca gcc aag aag ccc   4187
Asp Leu Arg Val Ser Ile Arg Pro Ala Pro Glu Thr Ala Lys Lys Pro
            1365             1370             1375


gag gaa gcc aag aat acc atg ttc ctt gaa atc tgc acc aag tac ttg   4235
Glu Glu Ala Lys Asn Thr Met Phe Leu Glu Ile Cys Thr Lys Tyr Leu
            1380             1385             1390


gga gat gtg gac gcc act atg tcc atc ctg gac atc tcc atg atg act   4283
Gly Asp Val Asp Ala Thr Met Ser Ile Leu Asp Ile Ser Met Met Thr
        1395             1400             1405


ggc ttt gct cca gac aca aag gac ctg gaa ctg ctg gcc tct gga gta   4331
```

```
    Gly Phe Ala Pro Asp Thr Lys Asp Leu Glu Leu Leu Ala Ser Gly Val
    1410                1415                1420                1425


    gat aga tac atc tcc aag tac gag atg aac aaa gcc ttc tcc aac aag    4379
    Asp Arg Tyr Ile Ser Lys Tyr Glu Met Asn Lys Ala Phe Ser Asn Lys
                        1430                1435                1440


    aac acc ctc atc atc tac cta gaa aag att tca cac acc gaa gaa gac    4427
    Asn Thr Leu Ile Ile Tyr Leu Glu Lys Ile Ser His Thr Glu Glu Asp
                    1445                1450                1455


    tgc ctg acc ttc aaa gtt cac cag tac ttt aat gtg gga ctt atc cag    4475
    Cys Leu Thr Phe Lys Val His Gln Tyr Phe Asn Val Gly Leu Ile Gln
                1460                1465                1470


    ccc ggg tcg gtc aag gtc tac tcc tat tac aac ctc gag gaa tca tgc    4523
    Pro Gly Ser Val Lys Val Tyr Ser Tyr Tyr Asn Leu Glu Glu Ser Cys
                1475                1480                1485


    acc cgg ttc tat cat cca gag aag gac gat ggg atg ctc agc aag ctg    4571
    Thr Arg Phe Tyr His Pro Glu Lys Asp Asp Gly Met Leu Ser Lys Leu
    1490                1495                1500                1505


    tgc cac agt gaa atg tgc cgg tgt gct gaa gag aac tgc ttc atg caa    4619
    Cys His Ser Glu Met Cys Arg Cys Ala Glu Glu Asn Cys Phe Met Gln
                        1510                1515                1520


    cag tca cag gag aag atc aac ctg aat gtc cgg cta gac aag gct tgt    4667
    Gln Ser Gln Glu Lys Ile Asn Leu Asn Val Arg Leu Asp Lys Ala Cys
                    1525                1530                1535


    gag ccc gga gtc gac tat gtg tac aag acc gag cta acc aac ata aag    4715
    Glu Pro Gly Val Asp Tyr Val Tyr Lys Thr Glu Leu Thr Asn Ile Lys
                1540                1545                1550


    ctg ttg gat gat ttt gat gag tac acc atg acc atc cag cag gtc atc    4763
    Leu Leu Asp Asp Phe Asp Glu Tyr Thr Met Thr Ile Gln Gln Val Ile
                1555                1560                1565


    aag tca ggc tca gat gag gtg cag gca ggg cag caa cgc aag ttc atc    4811
    Lys Ser Gly Ser Asp Glu Val Gln Ala Gly Gln Gln Arg Lys Phe Ile
    1570                1575                1580                1585


    agc cac atc aag tgc aga aac gcc ctg aag ctg cag aaa ggg aag aag    4859
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Ser His Ile Lys Cys Arg Asn Ala Leu Lys Leu Gln Lys Gly Lys Lys
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Tyr Leu Met Trp Gly Leu Ser Ser Asp Leu Trp Gly Glu Lys Pro Asn
            1605   1610   1615

acc agc tac atc att ggg aag gac acg tgg gtg gag cac tgg cct gag   4955
Thr Ser Tyr Ile Ile Gly Lys Asp Thr Trp Val Glu His Trp Pro Glu
            1620   1625   1630

gca gaa gaa tgc cag gat cag aag tac cag aaa cag tgc gaa gaa ctt   5003
Ala Glu Glu Cys Gln Asp Gln Lys Tyr Gln Lys Gln Cys Glu Glu Leu
            1635   1640   1645

ggg gca ttc aca gaa tct atg gtg gtt tat ggt tgt ccc aac tga   5048
Gly Ala Phe Thr Glu Ser Met Val Val Tyr Gly Cys Pro Asn
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atcgagtctc agctggtgtt cctataactc cgccccagct gacagcctac gtggtcaagg   360

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